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	10	20	30	40	50	
CPGbP656	1	MEGDGSDPEP	PDAGEDSKSE	NGENAPIYCI	CRKPDINCFM	IGCDNCNEWF
CPGbP241	1	-----	-----	-----	-----	-----
CPGbP181	1	-----	-----	-----	-----	-----
	60	70	80	90	100	
CPGbP656	51	HGDCIRITEK	MAKAIREWYC	RECREKDPKL	EIRYRHKKSR	ERDGNERDSS
CPGbP241	51	-----	-----	-----	-----	-----
CPGbP181	51	-----	-----	-----	-----	-----
	110	120	130	140	150	
CPGbP656	101	EPRDEGGGRK	RPVPDPNLQR	RAGSGTGVGA	MLARGSASPH	KSSPQPLVAT
CPGbP241	101	-----GGGRK	RPVPDPNLQR	RAGSGTGVGA	MLARGSASPH	KSSPQPLVAT
CPGbP181	101	-----GGGRK	RPVPDPNLQR	RAGSGTGVGA	MLARGSASPH	KSSPQPLVAT
	160	170	180	190	200	
CPGbP656	151	PSQHHQQQQQ	QIKRSARMCG	ECEACRRTED	CGHCDFCRDM	KKFGGPNKIR
CPGbP241	151	PSQHHQQQQQ	QIKRSARMCG	ECEACRRTED	CGHCDFCRDM	KKFGGPNKIR
CPGbP181	151	PSQHHQQQQQ	QIKRSARMCG	ECEACRRTED	CGHCDFCRDM	KKFGGPNKIR
	210	220	230	240	250	
CPGbP656	201	QKCRLRQCQL	RARESYKYFP	SSLSPVTPSE	SLPRRRRPLP	TQQQPQPSQK
CPGbP241	201	QKCRLRQCQL	RARESYKYFP	SSLSPVTPSE	SLPRRRRPLP	TQQQPQPSQK
CPGbP181	201	QKCRLRQCQL	RARESYKYFP	SSLSPVTPSE	SLPRRRRPLP	TQQQPQPSQK
	260	270	280	290	300	
CPGbP656	251	LGRIREDEGA	VASSTVKEPP	EATATPEPLS	DEDLPLDPDL	YQDFCAGAFD
CPGbP241	251	LGRIREDEGA	VASSTVKEPP	EATATPEPLS	DEDLPLDPDL	YQDFCAGAFD
CPGbP181	251	LGRIREDEGA	VASSTVKEPP	EATATPEPLS	DEDLPL----	-----
	310	320	330	340	350	
CPGbP656	301	DNGLPWMSDT	EESPFLDPAL	RKRAVKVKHV	KRREKKSEKK	KEERYKRHRQ
CPGbP241	301	DNGLPWMSDT	EESPFLDPAL	RKRAVKVKHV	KRREKKSEKK	KEERYK----
	360	370	380	390	400	
CPGbP656	351	KQKHKDKWKH	PERADAKDPA	SLPQCLGPGC	VRPAQPSSKY	CSDDCGMKLA
	410	420	430	440	450	
CPGbP656	401	ANRIYEILPQ	RIQQWQQSPC	IAEEHGKKLL	ERIRREQQSA	RTRLQEMERR
	460	470	480	490	500	
CPGbP656	451	FHELEAILLR	AKQQAVREDE	ESNEGSDDT	DLQIFCVSCG	HPINPRVALR
	510	520	530	540	550	
CPGbP656	501	HMERCYAKYE	SQTSFGSMYP	TRIEGATRLF	CDVYNPQSKT	YCKRLQVLCF
	560	570	580	590	600	
CPGbP656	551	EHSRDPKVPA	DEVCGCPLVR	DVFELTGDFC	RLPKRQCNRH	YCWEKLRAE
	610	620	630	640	650	
CPGbP656	601	VDLERVVRWY	KLDELFEQER	NVRTAMTNRA	GLLALMLHQT	IQHDPLTTDL
	660	670	680	690	700	
CPGbP656	651	RSSADR....

Fig. 1

Fig. 2

5'	ATG	GAG	GGA	GAT	GGT	TCA	GAC	CCA	GAG	CCT	CCA	GAT	GCC	GGG	GAG	GAC	AGC	AAG
	M	E	G	D	G	S	D	P	E	P	P	D	A	G	E	D	S	K
	TCC	GAG	AAT	GGG	GAG	AAT	GCG	CCC	ATC	TAC	TGC	ATC	TGC	CGC	AAA	CCG	GAC	ATC
	S	E	N	G	E	N	A	P	I	Y	C	I	C	R	K	P	D	I
	AAC	TGC	TTC	ATG	ATC	GGG	TGT	GAC	AAC	TGC	AAT	GAG	TGG	TTC	CAT	GGG	GAC	TGC
	N	C	F	M	I	G	C	D	N	C	N	E	W	F	H	G	D	C
	ATC	CGG	ATC	ACT	GAG	AAG	ATG	GCC	AAG	GCC	ATC	CGG	GAG	TGG	TAC	TGT	CGG	GAG
	I	R	I	T	E	K	M	A	K	A	I	R	E	W	Y	C	R	E
	TGC	AGA	GAG	AAA	GAC	CCC	AAG	CTA	GAG	ATT	CGC	TAT	CGG	CAC	AAG	AAG	TCA	CGG
	C	R	E	K	D	P	K	L	E	I	R	Y	R	H	K	K	S	R
	GAG	CGG	GAT	GGC	AAT	GAG	CGG	GAC	AGC	AGT	GAG	CCC	CGG	GAT	GAG	GGT	GGA	GGG
	E	R	D	G	N	E	R	D	S	S	E	P	R	D	E	G	G	G
																G	G	G
	CGC	AAG	AGG	CCT	GTC	CCT	GAT	CCA	AAC	CTG	CAG	CGC	CGG	GCA	GGG	TCA	GGG	ACA
	R	K	R	P	V	P	D	P	N	L	Q	R	R	A	G	S	G	T
	R	K	R	P	V	P	D	P	N	L	Q	R	R	A	G	S	G	T
	GGG	GTT	GGG	GCC	ATG	CTT	GCT	CGG	GGC	TCT	GCT	TCG	CCC	CAC	AAA	TCC	TCT	CCG
	G	V	G	A	M	L	A	R	G	S	A	S	P	H	K	S	S	P
	G	V	G	A	M	L	A	R	G	S	A	S	P	H	K	S	S	P
	CAG	CCC	TTG	GTG	GCC	ACA	CCC	AGC	CAG	CAT	CAC	CAG	CAG	CAG	CAG	CAG	CAG	ATC
	Q	P	L	V	A	T	P	S	Q	H	H	Q	Q	Q	Q	Q	Q	I
	Q	P	L	V	A	T	P	S	Q	H	H	Q	Q	Q	Q	Q	Q	I
	AAA	CGG	TCA	GCC	CGC	ATG	TGT	GGT	GAG	TGT	GAG	GCA	TGT	CGG	CGC	ACT	GAG	GAC
	K	R	S	A	R	M	C	G	E	C	E	A	C	R	R	T	E	D
	K	R	S	A	R	M	C	G	E	C	E	A	C	R	R	T	E	D

Fig. 2 (Continued)

		549			558			567			576			585			594	
TGT	GGT	CAC	TGT	GAT	TTC	TGT	CGG	GAC	ATG	AAG	AAG	TTC	GGG	GGC	CCC	AAC	AAG	
C	G	H	C	D	F	C	R	D	M	K	K	F	G	G	P	N	K	
C	G	H	C	D	F	C	R	D	M	K	K	F	G	G	P	N	K	
		603			612			621			630			639			648	
ATC	CGG	CAG	AAG	TGC	CGG	CTG	CGC	CAG	TGC	CAG	CTG	CGG	GCC	CGG	GAA	TCG	TAC	
I	R	Q	K	C	R	L	R	Q	C	Q	L	R	A	R	E	S	Y	
I	R	Q	K	C	R	L	R	Q	C	Q	L	R	A	R	E	S	Y	
		657			666			675			684			693			702	
AAG	TAC	TTC	CCT	TCC	TCG	CTC	TCA	CCA	GTG	ACG	CCC	TCA	GAG	TCC	CTG	CCA	AGG	
K	Y	F	P	S	S	L	S	P	V	T	P	S	E	S	L	P	R	
K	Y	F	P	S	S	L	S	P	V	T	P	S	E	S	L	P	R	
		711			720			729			738			747			756	
CCC	CGC	CGG	CCA	CTG	CCC	ACC	CAA	CAG	CAG	CCA	CAG	CCA	TCA	CAG	AAG	TTA	GGG	
P	R	R	P	L	P	T	Q	Q	Q	P	Q	P	S	Q	K	L	G	
P	R	R	P	L	P	T	Q	Q	Q	P	Q	P	S	Q	K	L	G	
		765			774			783			792			801			810	
CGC	ATC	CGT	GAA	GAT	GAG	GGG	GCA	GTG	GCG	TCA	TCA	ACA	GTC	AAG	GAG	CCT	CCT	
R	I	R	E	D	E	G	A	V	A	S	S	T	V	K	E	P	P	
R	I	R	E	D	E	G	A	V	A	S	S	T	V	K	E	P	P	
		819			828			837			846			855			864	
GAG	GCT	ACA	GCC	ACA	CCT	GAG	CCA	CTC	TCA	GAT	GAG	GAC	CTA	CCT	CTG	GAT	CCT	
E	A	T	A	T	P	E	P	L	S	D	E	D	L	P	L	D	P	
E	A	T	A	T	P	E	P	L	S	D	E	D	L	P	L			
		873			882			891			900			909			918	
GAC	CTG	TAT	CAG	GAC	TTC	TGT	GCA	GGG	GCC	TTT	GAT	GAC	AAT	GGC	CTG	CCC	TGG	
D	L	Y	Q	D	F	C	A	G	A	F	D	D	N	G	L	P	W	
		927			936			945			954			963			972	
ATG	AGC	GAC	ACA	GAA	GAG	TCC	CCA	TTC	CTG	GAC	CCC	GCG	CTG	CGG	AAG	AGG	GCA	
M	S	D	T	E	E	S	P	F	L	D	P	A	L	R	K	R	A	
		981			990			999			1008			1017			1026	
GTG	AAA	GTG	AAG	CAT	GTG	AAG	CGT	CGG	GAG	AAG	AAG	TCT	GAG	AAG	AAG	AAG	GAG	
V	K	V	K	H	V	K	R	R	E	K	K	S	E	K	K	K	E	
		1035			1044			1053			1062			1071			1080	
GAG	CGA	TAC	AAG	CGG	CAT	CGG	CAG	AAG	CAG	AAG	CAC	AAG	GAT	AAA	TGG	AAA	CAC	
E	R	Y	K	R	H	R	Q	K	Q	K	H	K	D	K	W	K	H	
		1089			1098			1107			1116			1125			1134	
CCA	GAG	AGG	GCT	GAT	GCC	AAG	GAC	CCT	GCG	TCA	CTG	CCC	CAG	TGC	CTG	GGG	CCC	
P	E	R	A	D	A	K	D	P	A	S	L	P	Q	C	L	G	P	

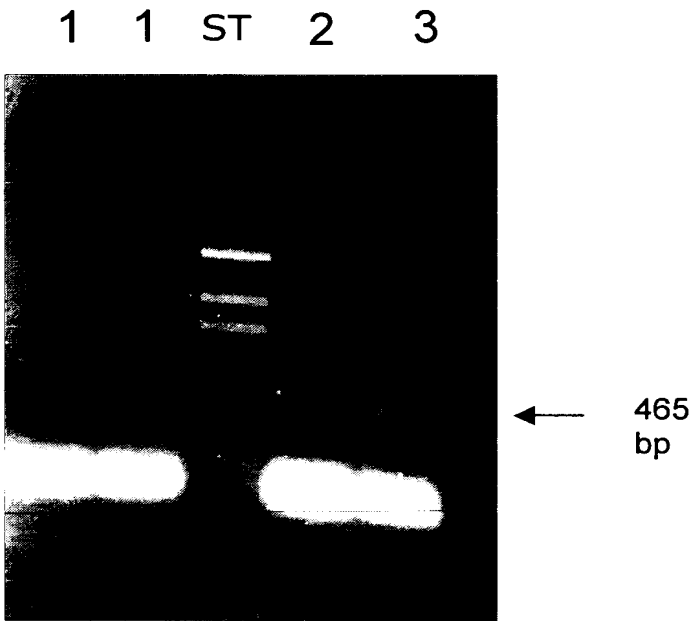
Fig. 2 (Continued)

1143	1152	1161	1170	1179	1188
GGC TGT GTG CGC CCC GCC CAG CCC AGC TCC AAG TAT TGC TCA GAT GAC TGT GGC					
G C V R P A Q P S S K Y C S D D C G					
1197	1206	1215	1224	1233	1242
ATG AAG CTG GCA GCC AAC CGC ATC TAC GAG ATC CTC CCC CAG CGC ATC CAG CAG					
M K L A A N R I Y E I L P Q R I Q Q					
1251	1260	1269	1278	1287	1296
TGG CAG CAG AGC CCT TGC ATT GCT GAA GAG CAC GGC AAG AAG CTG CTC GAA CGC					
W Q Q S P C I A E E H G K K L L E R					
1305	1314	1323	1332	1341	1350
ATT CGC CGA GAG CAG CAG AGT GCC CGC ACC CGC CTT CAG GAA ATG GAA CGC CGA					
I R R E Q Q S A R T R L Q E M E R R					
1359	1368	1377	1386	1395	1404
TTC CAT GAG CTT GAG GCC ATC ATT CTA CGT GCC AAG CAG CAG GCT GTG CGC GAG					
F H E L E A I I L R A K Q Q A V R E					
1413	1422	1431	1440	1449	1458
GAT GAG GAG AGC AAC GAG GGT GAC AGT GAT GAC ACA GAC CTG CAG ATC TTC TGT					
D E E S N E G D S D D T D L Q I F C					
1467	1476	1485	1494	1503	1512
GTT TCC TGT GGG CAC CCC ATC AAC CCA CGT GTT GCC TTG CGC CAC ATG GAG CGC					
V S C G H P I N P R V A L R H M E R					
1521	1530	1539	1548	1557	1566
TGC TAC GCC AAG TAT GAG AGC CAG ACG TCC TTT GGG TCC ATG TAC CCC ACA CGC					
C Y A K Y E S Q T S F G S M Y P T R					
1575	1584	1593	1602	1611	1620
ATT GAA GGG GCC ACA CGA CTC TTC TGT GAT GTG TAT AAT CCT CAG AGC AAA ACA					
I E G A T R L F C D V Y N P Q S K T					
1629	1638	1647	1656	1665	1674
TAC TGT AAG CGG CTC CAG GTG CTG TGC CCC GAG CAC TCA CGG GAC CCC AAA GTG					
Y C K R L Q V L C P E H S R D P K V					
1683	1692	1701	1710	1719	1728
CCA GCT GAC GAG GTA TGC GGG TGC CCC CTT GTA CGT GAT GTC TTT GAG CTC ACG					
P A D E V C G C P L V R D V F E L T					
1737	1746	1755	1764	1773	1782
GGT GAC TTC TGC CGC CTG CCC AAG CGC CAG TGC AAT CGC CAT TAC TGC TGG GAG					
G D F C R L P K R Q C N R H Y C W E					

Fig. 2 (Continued)

1791				1800			1809			1818			1827			1836	
AAG	CTG	CGG	CGT	GCG	GAA	GTG	GAC	TTG	GAG	CGC	GTG	CGT	GTG	TGG	TAC	AAG	CTG
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
K	L	R	R	A	E	V	D	L	E	R	V	R	V	W	Y	K	L
1845				1854			1863			1872			1881			1890	
GAC	GAG	CTG	TTT	GAG	CAG	GAG	CGC	AAT	GTG	CGC	ACA	GCC	ATG	ACA	AAC	CGC	GCG
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
D	E	L	F	E	Q	E	R	N	V	R	T	A	M	T	N	R	A
1899				1908			1917			1926			1935			1944	
GGA	TTG	CTG	GCC	CTG	ATG	CTG	CAC	CAG	ACG	ATC	CAG	CAC	GAT	CCC	CTC	ACT	ACC
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
G	L	L	A	L	M	L	H	Q	T	I	Q	H	D	P	L	T	T
1953				1962			1971										
GAC	CTG	CGC	TCC	AGT	GCC	GAC	CGC	TGA	3'								
---	---	---	---	---	---	---	---	---	---								
D	L	R	S	S	A	D	R	*									

Figure 3



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Figure 4

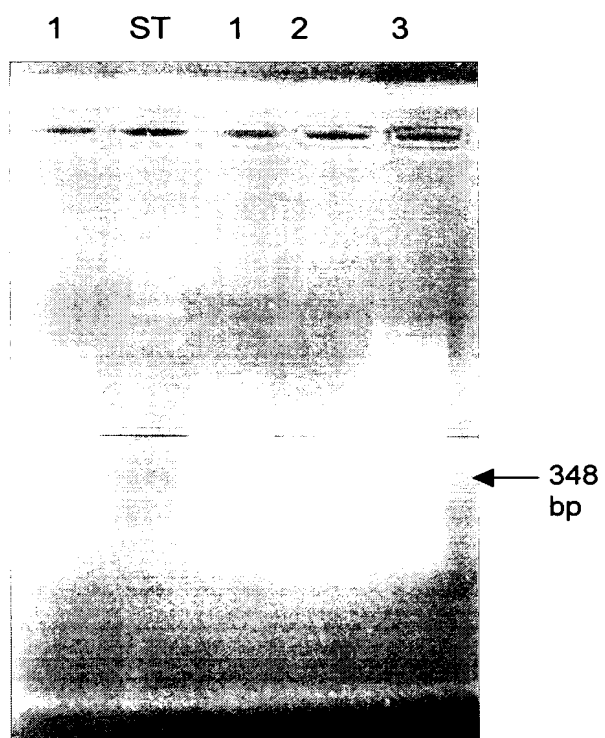


Figure 5

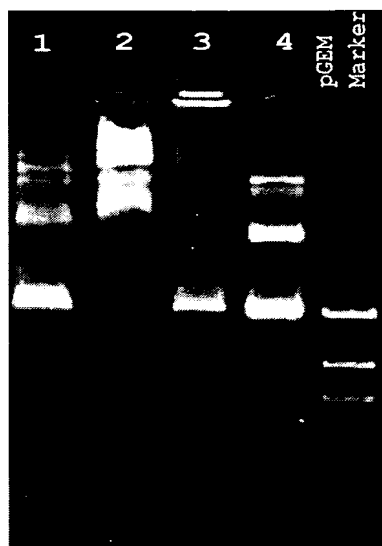
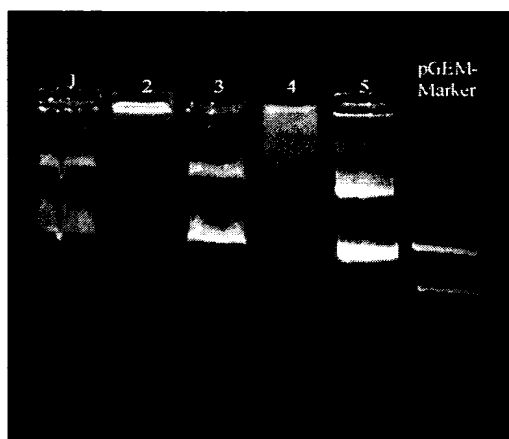
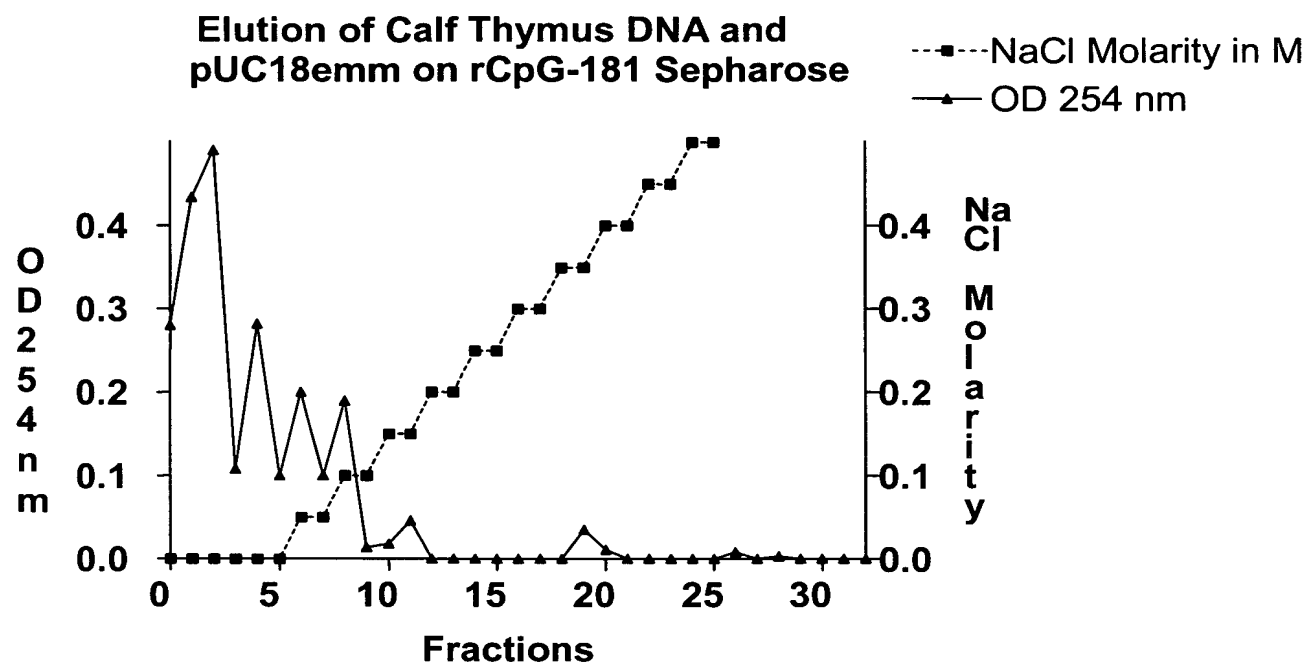


Figure 6



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Figure 7



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Figure 8

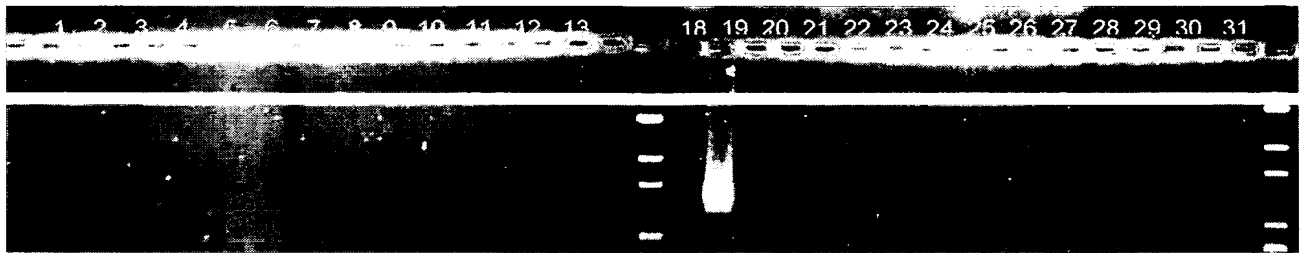
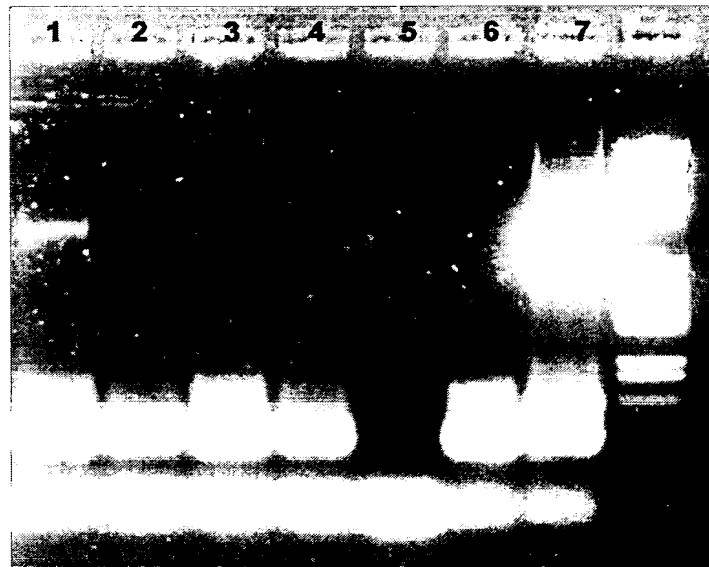


Figure 9

Results of PCR after enrichment of prokaryotic DNA
from a DNA mixture of *Staphylococcus aureus* and human DNA
using coupled CpGbP-181 protein on CNBr sepharose

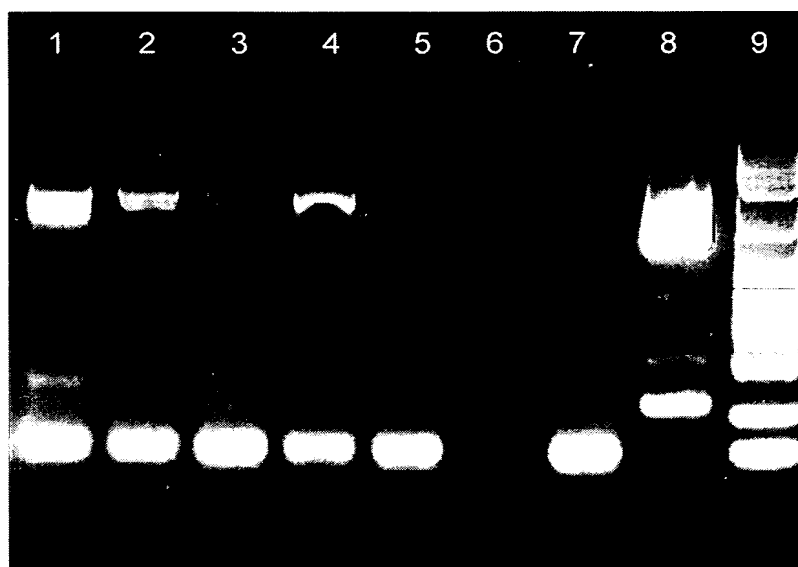


Legend:

- | | |
|--|-------------------|
| 1 E ₁ (E= elution fraction) | 6 prior to column |
| 2 E ₂ | 7 pos. control |
| 3 E ₃ | 8 pGEM marker |
| 4 E ₄ | |
| 5 E ₅ | |

Figure 10

Results of PCR after enrichment of prokaryotic DNA from a DNA mixture of *Staphylococcus aureus* and human DNA using coupled CpG-181 protein on AH sepharose



Legend:

1 E ₁ (E= elution fraction)	6	negative control
2 E ₂	7	prior to column
3 E ₃	8	positive control
4 E ₄	9	BIORAD marker
5 E ₅		